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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/518,763DATE: 03/23/2000
TIME: 12:19:31

Input Set: I518763.RAW

This Raw Listing contains the General Information
Section and up to first 5 pages.

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1 <110> APPLICANT: Blissard, Gary W.
2 Granados, Robert R.
3 Lin, Guangyun
4 <120> TITLE OF INVENTION: STABLE CELL LINES RESISTANT TO APOPTOSIS AND NUTRIENT
5 STRESS AND METHODS OF MAKING SAME
6 <130> FILE REFERENCE: BTI44
7 <140> CURRENT APPLICATION NUMBER: US/09/518,763
8 <141> CURRENT FILING DATE: 2000-03-03
9 <160> NUMBER OF SEQ ID NOS: 7
10 <170> SOFTWARE: PatentIn Ver. 2.0
11 <210> SEQ ID NO 1
12 <211> LENGTH: 900
13 <212> TYPE: DNA
14 <213> ORGANISM: Autographa californica nucleopolyhedrovirus
15 <220> FEATURE:
16 <221> NAME/KEY: CDS
17 <222> LOCATION: (1)..(897)
18 <300> PUBLICATION INFORMATION:
19 <301> AUTHORS: Ayres, Martin D.
Howard, Stephen C.
Kuzio, John
Lopez-Ferber, Miguel
Possee, Robert D.
20 <302> TITLE: The Complete DNA Sequence of Autographa californica
Nuclear Polyhedrosis Virus
21 <303> JOURNAL: Virology
22 <304> VOLUME: 202
23 <305> ISSUE: 2
24 <306> PAGES: 586-605
25 <307> DATE: 1994
26 <308> DATABASE ACCESSION NUMBER: L22858
27 <309> DATABASE ENTRY DATE: 1999-03-08
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32 1 5 10 15
33 cga gat tgt cag gtg gac aaa caa acc aga gag ttg gtg tac att aac 96
34 Arg Asp Cys Gln Val Asp Lys Gln Thr Arg Glu Leu Val Tyr Ile Asn
35 20 25 30
36 aag att atg aac acg caa ttg aca aaa ccc gtt ctc atg atg ttt aac 144
37 Lys Ile Met Asn Thr Gln Leu Thr Lys Pro Val Leu Met Met Phe Asn
38 35 40 45
39 att tcg ggt cct ata cga agc gtt acg cgc aag aac aac aat ttg cgc 192
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45 Ile Ser Gly Pro Ile Arg Ser Val Thr Arg Lys Asn Asn Asn Leu Arg
 46 50 55 60
 47 gac aga ata aaa tca aaa gtc gat gaa caa ttt gat caa cta gaa cgc 240
 48 Asp Arg Ile Lys Ser Lys Val Asp Glu Gln Phe Asp Gln Leu Glu Arg
 49 65 70 75 80
 50 gat tac agc gat caa atg gat gga ttc cac gat agc atc aag tat ttt 288
 51 Asp Tyr Ser Asp Gln Met Asp Gly Phe His Asp Ser Ile Lys Tyr Phe
 52 85 90 95
 53 aaa gat gaa cac tat tcg gta agt tgc caa aat ggc agc gtg ttg aaa 336
 54 Lys Asp Glu His Tyr Ser Val Ser Cys Gln Asn Gly Ser Val Leu Lys
 55 100 105 110
 56 agc aag ttt gct aaa att tta aag agt cat gat tat acc gat aaa aag 384
 57 Ser Lys Phe Ala Lys Ile Leu Lys Ser His Asp Tyr Thr Asp Lys Lys
 58 115 120 125
 59 tct att gaa gct tac gag aaa tac tgt ttg ccc aaa ttg gtc gac gaa 432
 60 Ser Ile Glu Ala Tyr Glu Lys Tyr Cys Leu Pro Lys Leu Val Asp Glu
 61 130 135 140
 62 cgc aac gac tac tac gtg gcg gta tgc gtg ttg aag ccg gga ttt gag 480
 63 Arg Asn Asp Tyr Tyr Val Ala Val Cys Val Leu Lys Pro Gly Phe Glu
 64 145 150 155 160
 65 aac ggc agc aac caa gtg cta tct ttc gag tac aac ccg att ggt aac 528
 66 Asn Gly Ser Asn Gln Val Leu Ser Phe Glu Tyr Asn Pro Ile Gly Asn
 67 165 170 175
 68 aaa gtt att gtg ccg ttt gct cac gaa att aac gac acg gga ctt tac 576
 69 Lys Val Ile Val Pro Phe Ala His Glu Ile Asn Asp Thr Gly Leu Tyr
 70 180 185 190
 71 gag tac gac gtc gta gct tac gtg gac agt gtg cag ttt gat ggc gaa 624
 72 Glu Tyr Asp Val Val Ala Tyr Val Asp Ser Val Gln Phe Asp Gly Glu
 73 195 200 205
 74 caa ttt gaa gag ttt gtg cag agt tta ata ttg ccg tcg tcg ttc aaa 672
 75 Gln Phe Glu Glu Phe Val Gln Ser Leu Ile Leu Pro Ser Ser Phe Lys
 76 210 215 220
 77 aat tcg gaa aag gtt tta tat tac aac gaa gcg tcg aaa aac aaa agc 720
 78 Asn Ser Glu Lys Val Leu Tyr Tyr Asn Glu Ala Ser Lys Asn Lys Ser
 79 225 230 235 240
 80 atg atc tac aag gct tta gag ttt act aca gaa tcg agc tgg ggc aaa 768
 81 Met Ile Tyr Lys Ala Leu Glu Phe Thr Thr Glu Ser Ser Trp Gly Lys
 82 245 250 255
 83 tcc gaa aag tat aat tgg aaa att ttt tgt aac ggt ttt att tat gat 816
 84 Ser Glu Lys Tyr Asn Trp Lys Ile Phe Cys Asn Gly Phe Ile Tyr Asp
 85 260 265 270
 86 aaa aaa tca aaa gtg ttg tat gtt aaa ttg cac aat gta act agt gca 864
 87 Lys Lys Ser Lys Val Leu Tyr Val Lys Leu His Asn Val Thr Ser Ala
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 93 <211> LENGTH: 299
 94 <212> TYPE: PRT

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101 Lys Ile Met Asn Thr Gln Leu Thr Lys Pro Val Leu Met Met Phe Asn
102 35 40 45
103 Ile Ser Gly Pro Ile Arg Ser Val Thr Arg Lys Asn Asn Asn Leu Arg
104 50 55 60
105 Asp Arg Ile Lys Ser Lys Val Asp Glu Gln Phe Asp Gln Leu Glu Arg
106 65 70 75 80
107 Asp Tyr Ser Asp Gln Met Asp Gly Phe His Asp Ser Ile Lys Tyr Phe
108 85 90 95
109 Lys Asp Glu His Tyr Ser Val Ser Cys Gln Asn Gly Ser Val Leu Lys
110 100 105 110
111 Ser Lys Phe Ala Lys Ile Leu Lys Ser His Asp Tyr Thr Asp Lys Lys
112 115 120 125
113 Ser Ile Glu Ala Tyr Glu Lys Tyr Cys Leu Pro Lys Leu Val Asp Glu
114 130 135 140
115 Arg Asn Asp Tyr Tyr Val Ala Val Cys Val Leu Lys Pro Gly Phe Glu
116 145 150 155 160
117 Asn Gly Ser Asn Gln Val Leu Ser Phe Glu Tyr Asn Pro Ile Gly Asn
118 165 170 175
119 Lys Val Ile Val Pro Phe Ala His Glu Ile Asn Asp Thr Gly Leu Tyr
120 180 185 190
121 Glu Tyr Asp Val Val Ala Tyr Val Asp Ser Val Gln Phe Asp Gly Glu
122 195 200 205
123 Gln Phe Glu Glu Phe Val Gln Ser Leu Ile Leu Pro Ser Ser Phe Lys
124 210 215 220
125 Asn Ser Glu Lys Val Leu Tyr Tyr Asn Glu Ala Ser Lys Asn Lys Ser
126 225 230 235 240
127 Met Ile Tyr Lys Ala Leu Glu Phe Thr Thr Glu Ser Ser Trp Gly Lys
128 245 250 255
129 Ser Glu Lys Tyr Asn Trp Lys Ile Phe Cys Asn Gly Phe Ile Tyr Asp
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140 <223> OTHER INFORMATION: Description of Artificial Sequence:
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176 <223> OTHER INFORMATION: Description of Artificial Sequence:
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**VERIFICATION SUMMARY
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Line ? Error/Warning

Original Text
